I claim:

1. A method of quantitatively analyzing a sample analyte, comprising:

performing matrix-assisted laser desorption ionization mass spectrometry on the sample analyte and an internal standard, and comparing the mass spectrometry of the sample analyte with the mass spectrometry of the internal standard without the use of calibration curves.

2. The method of claim 1, wherein the concentrations, peak intensities and molecular weight of the sample analyte and internal standard are compared.

3. The method of claim 1, wherein the sample analyte is a biomolecule.

4. The method of claim 3, wherein the sample analyte is selected from peptides, proteins and digest fragments of sample peptide or sample protein.

5. The method of claim 3, wherein the sample analyte is selected from DNA, t-RNA, m-RNA or r-RNA or sample digest fragments.

6. The method of claim 3, wherein the sample analyte is selected from derivatives of sample analytes in claims 4 and 5.

7. The method of claim 1, wherein the internal standard is selected from a biomolecule and a synthetic molecule.

8. The method of claim 1, wherein the sample analyte and the internal standard are compared according to the following equation:

$$(MW(Sample) \times \sum I(Sample)) / [Sample] = (MW(IS) \times \sum I(IS)) / [IS]$$

where MW designates molecular weight, $\sum I$ designates sum of peak intensities, brackets designate concentration, and IS designates internal standard.

9. The method of claim 8, wherein the sample analyte and the internal standard are each a biomolecule that ionizes, upon application of the matrix-assisted laser desorption ionization, primarily on a same functional group.

10. The method of claim 2 , wherein the sample analyte and the internal standard are compared according to the following equation:

$$(MW(Sample) \times I(Sample)) / [Sample] = (MW(IS) \times I(IS)) / [IS]*C$$

where MW designates molecular weight, I designates peak intensity, brackets designate concentration, and IS designates internal standard and C represent a constant.

11. The method of claim 10, wherein the sample analyte and the internal standard are each proteins that ionize, upon application of the matrix-assisted laser desorption ionization, on different functional group where the constant C corrects for ionization efficiencies.

12. The method of claim 1, wherein matrix-assisted laser desorption ionization time-of-flight mass spectrometry is performed on the sample analyte.

13. A method of quantitatively evaluating biomolecular interactions, comprising:

performing matrix-assisted laser desorption ionization mass spectrometry on a sample analyte(s) and an internal standard, and comparing the mass spectrometry of the sample analyte with the mass spectrometry of the internal standard.

14. The method of claim 13, wherein the matrix-assisted laser desorption ionization mass spectrometry is performed on a sample analyte on or in a biomaterial.

15. The method of claim 14, wherein the biomaterial is a contact lens, an intraocular lens, or a drug delivery device.

16. The method of claim 13, for quantifying analytes that are differentially present in a first and second biological sample comprising the steps of:

a. selecting a plurality of different selectivity conditions to which the first and second samples will be exposed, wherein each selectivity condition is defined by an adsorbent and an eluant, and each different selectivity condition comprises a different adsorbent and the same or different eluant, and the samples are exposed to a selectivity condition by contacting a sample with an adsorbent and washing the adsorbent with an eluant to allow retention of analytes in the sample by the adsorbent;

b. quantitatively detecting analytes in the first sample by exposing the first sample, in parallel, to each of the different selectivity conditions, and detecting analytes retained by the adsorbents by desorption spectrometry, wherein desorption spectrometry comprises desorbing and ionizing the analyte from the adsorbent with an energy source and detecting the desorbed and ionized analytes with a detector;

c. quantitatively detecting analytes in the second sample by exposing the second sample, in parallel, to each of the different selectivity conditions, and detecting analytes retained by the adsorbents by desorption spectrometry; and

d. comparing the analytes detected in the first biological sample with analytes detected in the second biological sample to identify analytes that are differentially present in the first and second biological sample.

17. The method of claim 16 wherein the adsorbent is provided in the form of a probe removably insertable in a desorption spectrometer, wherein the probe comprises a substrate having a surface and the adsorbent is attached to the surface at a predetermined location which is addressable by the energy source.

18. The method of claim 17 wherein the adsorbent is provided in the form of a bead comprising a solid phase to which the adsorbent is attached, and after contacting the sample with the adsorbent, the bead is placed on a surface of a probe removably insertable in a desorption spectrometer, at a predetermined location on the surface that is addressable by the energy source.

19. The method of claim 18 wherein at least two of the adsorbents are differently selected from the group consisting of a hydrophobic adsorbent, a thiophilic adsorbent, a normal phase adsorbent, an anionic adsorbent, a cationic adsorbent, a metal ion adsorbent and a glycoprotein interaction adsorbent.

20. The method of claim 16 wherein each adsorbent is washed with an eluant selected from the group consisting of a pH-based eluant, an ionic-strength-based eluant, a water structure-based eluant, a detergent-based eluant and a hydrophobicity-based eluant.

21. The method of claim 16 comprising selecting at least four different selectivity conditions defined by adsorbents, said absorbents selected from the group consisting of a hydrophobic adsorbent, a thiophilic adsorbent, a normal phase adsorbent, an anionic adsorbent, a cationic adsorbent, a metal ion adsorbent and a glycoprotein interaction adsorbent.

22. A method of quantitatively evaluating biomolecular and drug interactions, comprising performing matrix-assisted laser desorption ionization mass spectrometry on a sample analyte(s) and an internal standard, and comparing the mass spectrometry of the sample analyte with the mass spectrometry of the internal standard.

23. The method of claim 22 wherein the biomolecular and drug interactions occur in-vivo or from extracted in-vivo samples.

24. The method of claim 26 wherein the biomolecular and drug interactions occur in-vitro.

25. The method of claim 26 wherein the biomolecular and drug interactions are those that occur in the ocular environment.

26. The method of claim 22, wherein the evaluating is performed as a function of time to evaluate kinetics.